#5

Sequence Listing

<110> Syngenta Biotechnology, Inc.
Grina, Jonas

<120> NOVEL CYANOENAMINES USEFUL AS LIGANDS FOR MODULATING GENE EXPRESSION IN PLANTS OR ANIMALS

<130> 1392/2/2

<140> US/10/083,842

<141> 2002-02-27

<150> 60/272,905

<151> 2001-03-02

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<170> PatentIn version 3.0

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cttcggattg tgttgtgact gaaaagcgac gcgtatcgtg gtcgaagatt ctctataagt 180

gcataatata ttcgagacag tggatagcga ttcgtttcgg tttcatcgcg cggatgagtg 240

gttcatgccc gtagagacgc gtttagatag ttatggcgag gaaaaagtga agtgaaagcc 300

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atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt 408
Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe
1 5 10 15

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Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Phe Gly Met Pro
            20                  25                  30

gcg gcc atg gta atg tca ccg gag tcg ctg gcg tcg cca gag tac ggc      504
Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
        35                  40                  45

ggc ctc gag ctc tgg agc tac gat gag acc atg aca aac tat ccg gcg      552
Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
    50                  55                  60

cag tca ctg ctc ggc gcg tgt aat gcg ccg cag cag cag cag caa cag      600
Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln
65                  70                  75                  80

caa caa cag cag ccg tcc gct cag ccg ctg ccg tct atg ccg ctg ccg      648
Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
                85                  90                  95

atg cct cct aca act cct aaa tca gag aac gag tcc atg tcg tca ggt      696
Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
            100                 105                 110

cga gaa gaa tta tca ccg gcc tca agt ata aat gga tgt agt act gat      744
Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
        115                 120                 125

ggg gaa cca aga cga cag aag aaa ggg cca gcg ccg cgc cag cag gag      792
Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
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gaa ctg tgc ctt gtt tgc ggc gac agg gct tcg gga tat cac tat aac      840
Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
145                 150                 155                 160

gcg ctt acg tgc gaa gga tgt aaa ggg ttc ttc agg cgg agt gtg acc      888
Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
                165                 170                 175

aag aat gcg gta tat att tgt aaa ttt gga cac gcc tgc gag atg gac      936
Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
            180                 185                 190

atg tac atg agg aga aaa tgc caa gag tgt cgg ttg aag aaa tgc ctc      984
Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
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gcg gtg ggc atg agg ccc gag tgc gtc gtc cca gag tcc acg tgc aag     1032
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aac aaa aga aga gaa aag gaa gca cag aga gaa aaa gac aaa ctg cca     1080
Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
225                 230                 235                 240

gtc agt acg acg aca gtg gac gat cat atg cct gcc ata atg caa tgt     1128
Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
                245                 250                 255
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gac cct ccg ccc cca gag gcg gca agg att cac gaa gtg gtc ccg agg      1176
Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
            260                 265                 270

ttc cta acg gag aag cta atg gag cag aac aga ctg aag aat gtg acg      1224
Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
        275                 280                 285

ccg ctg tcg gcg aac cag aag tcc ctg atc gcg agg ctc gtg tgg tac      1272
Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
    290                 295                 300

cag gag ggg tac gag cag ccg tcg gag gaa gat ctc aag aga gtt aca      1320
Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
305                 310                 315                 320

cag aca tgg cag tta gaa gaa gaa gaa gag gag gaa act gac atg ccc      1368
Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
                325                 330                 335

ttc cgt cag atc aca gag atg acg atc tta aca gtg cag ctt att gta      1416
Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
            340                 345                 350

gaa ttc gca aag gga cta ccg gga ttc tcc aag ata tct cag tcc gat      1464
Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
        355                 360                 365

caa att aca tta tta aag gcg tca tca agc gaa gtg atg atg ctg cga      1512
Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
    370                 375                 380

gtg gcg cga cgg tac gac gcg gcg acg gac agc gtg ctg ttc gcg aac      1560
Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
385                 390                 395                 400

aac cag gcg tac acg cgc gac aac tac cgc aag gcg ggc atg tcc tac      1608
Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
                405                 410                 415

gtc atc gag gac ctg ctg cac ttc tgt cgg tgt atg tac tcc atg agc      1656
Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
            420                 425                 430

atg gac aat gtg cac tac gcg ctg ctc acc gcc atc gtt ata ttc tca      1704
Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser
        435                 440                 445

gac cgg cca ggc ctc gag caa ccc ctt tta gtg gag gaa atc cag aga      1752
Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg
    450                 455                 460

tac tac ttg aag acg ctg cgg gtt tac att tta aat cag cac agc gcg      1800
Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala
465                 470                 475                 480

tcg cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg      1848
Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr
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aag ctg aag aac agg aaa ctt ccg cca ttc ctc gag gag atc tgg gac 1944
Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp
515 520 525

gtg gcc gaa gtg tcg acg acg cag ccg acg ccg ggg gtg gcg gcg cag 1992
Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln
530 535 540

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Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu
545 550 555

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35 40 45

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Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
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Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln
65                  70                  75                  80

Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
                85                  90                  95

Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
            100                 105                 110

Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
        115                 120                 125

Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
    130                 135                 140

Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
145                 150                 155                 160

Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
                165                 170                 175

Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
            180                 185                 190

Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
        195                 200                 205

Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys
    210                 215                 220

Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
225                 230                 235                 240

Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
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Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
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Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
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Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
290                 295                 300

Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
305                 310                 315                 320

Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
            325                 330                 335

Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
        340                 345                 350

Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
    355                 360                 365

Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
370                 375                 380

Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
385                 390                 395                 400

Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
            405                 410                 415

Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
        420                 425                 430

Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser
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Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg
450                 455                 460

Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala
465                 470                 475                 480

Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr
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Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu
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Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp
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